

PEM's
Corr pLX

25 (PEM3) + 47 (PEM6) are first are G3

Table 1. Previously characterized and novel Pan Endothelial Markers. The most abundant tags derived by summing the tags from Normal EC (N-EC's) and Tumor EC (T-EC's) SAGE libraries are listed in descending order. N-EC and T-EC SAGE libraries contained 88,684 and 86,568 SAGE tags respectively. For comparison, the corresponding number of SAGE tags found in cultured human umbilical vein endothelial cells (HUEVC), human dermal microvascular endothelial cells (HMVEC), and non-endothelial cell lines (Cell Lines) are shown. The HUEVC SAGE library contained 290,000 tags and the HMVEC library 111,000 tags. Non-endothelial cell lines consisted of 1.8x10⁶ tags derived from a total of 14 different cancer cell lines including colon, breast, lung, and pancreatic cancers, as well as one non-transformed keratinocyte cell line, two kidney epithelial cell lines, and normal monocytes. Tag numbers for each group were normalized to 100,000 transcripts. A 'Description' of the gene product corresponding to each tag is given, followed by alternative names in parenthesis. The sequence CATG precedes all tags and the 15th base (11th shown) was determined as previously described by Veliculescu et al. (Nat Genet 1989 Dec;9(4):387-8).

no.	Tag Sequence	N-EC's	T-EC's	HUEVC	HMVEC	Cell Lines	Description
1	CATATCATTA	247	501	130	87	2	angiomodulin (ANG), IgFBP-7, IgFBP-P1, Mac25, TAF)
2	TGCACTTCAAG	328	141	0	0	0	hevin
3	TTTGACACTT	165	84	191	115	4	connective tissue growth factor (CTGF, IgFBP-P2)
4	CCCTTGTCGG	131	104	1	1	0	ESTs
5	TTGCTGACCTT	73	131	2	14	1	collagen, type VI, alpha 1
6	ACCATGGATT	102	67	0	0	2	interferon induced transmembrane protein 1 (IFIT-1, Leu 13)
7	ACACTCTTC	104	44	60	62	2	guanine nucleotide binding protein 11
8	TTCTGCTCTTG	71	67	118	72	0	Willebrand factor
9	TCCTGGCAGA	68	3	13	3	3	cysteine-rich protein 2 (CRP-2, ESP-1, SmILIM)
10	TAATCCCTAAG	26	108	34	18	1	collagen, type XVII, alpha 1
11	ATGCTTTCT	58	65	17	17	3	insulin-like growth factor-binding protein 4
12	GGGATAAAAGC	40	67	30	14	2	CD146 (S-Endo 1, P11H2, Muc18, MCAM, Mel-CAM)
13	TAGTGTCGTA	38	69	9	13	0	SPARC (osteonectin, BM-40)
14	TTCCTCCAAAT	20	86	16	64	2	collagen, type IV, alpha 2
15	GTGCTAAGCG	24	74	0	10	2	collagen, type VI, alpha 2
16	GTTTATGGATA	35	68	11	11	1	matrix Glu protein (MGP)
17	CCCTTGCAC	52	33	0	0	0	ESTs, Weakly similar to HPBRII-7 protein
18	TGTTCTGAGA	58	27	18	56	2	gap junction protein, alpha 1, 43kD (connexin 43)
19	AAGATCAAGT	34	50	2	4	1	actin, alpha 1, skeletal muscle / actin, alpha 2, smooth muscle, actin
20	TCTCTGAGCAT	32	48	0	0	0	aggrecanase 1 (metalloproteinase with thrombospondin type 1 motifs, 4)
21	CAGGTTCATA	22	56	0	0	0	small inducible cytokines subfamily B (Cys-X-Cys), member 14 (BRAK)
22	GCACAACATTCT	43	25	6	22	0	calcitonin receptor-like receptor activity modifying protein 2
23	AGCTTGTGCC	45	23	0	0	0	calcitonin receptor-like receptor activity modifying protein 3
24	CTTCGGATAA	13	54	12	0	0	cell division cycle 42 (GTP-binding protein, 25kD)
25	GAACATAATA	42			13	6	ESTs

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64 CAGATGGAGGC	18	10	1	9	0	ESTs
65 AGGCTCCCTGGC	8	20	0	0	0	ESTs
66 TCTGCTCTCTAG	20	8	40	15	0	ESTs
67 GCCTTAGGATG	18	9	10	14	0	ESTs
68 GGTGGTCGCG	6	21	0	0	1	ESTs
69 ACAACTACCCA	5	22	4	5	0	P311 protein
70 CTTCCTCTGAG	18	9	1	4	1	basic transcription element binding protein 1
71 GCTAAATAATGT	10	17	0	2	0	KIAA0777 protein
72 TGTCGTTTTT	10	15	1	4	0	KIAA0758 protein / protein kinase, cAMP-dependent, catalytic, alpha
73 CATGAGGGATC	17	8	0	1	0	Interleukin 1 receptor, type I
74 GCAGCAGGCCAC	6	18	0	2	0	T-box 2
75 TGACTGTATT	13	11	0	0	0	ESTs / amine oxidase, copper containing 3 (vascular adhesion protein 1)
76 GAATGCTCTTG	6	18	0	11	0	g9 junction protein, alpha 4, 37kD (connexin 37)
77 GTAGTCTTGG	18	6	0	5	0	ESTs, clone 236598 mRNA
78 TCCGCTCTCTCC	6	17	0	0	0	periodontal ligament fibroblast protein
79 GGCGATGGCT	5	18	12	5	0	ESTs, DKFZP086B0621 protein
80 AAATATGTGTT	19	4	13	3	0	ESTs
81 GTCATTTCTTA	11	11	10	2	0	transcription factor 8 (represses interleukin 2 expression)
82 CTCCTCCAAACC	14	8	0	0	0	complement component 1 inhibitor (angioedema, hereditary)
83 TTAAATGTAA	4	18	0	0	0	guanylate cyclase 1, soluble, beta 3
84 TCAAGCATCA	13	9	0	1	0	ESTs
85 GAAGACACTTG	15	7	1	0	0	ESTs
86 GGTTAGGGTGA	6	15	0	0	1	Integrin, alpha 7
87 TGGAAACAGTGA	10	10	10	5	0	ESTs
88 GAGTGGCTAGC	10	9	0	0	0	ESTs
89 GTCAAGGGTCC	13	7	0	9	0	decidual protein induced by progesterone
90 GTCACTGACTT	14	6	4	1	0	halvy (Drosophila)-homolog
91 AGCAGAGACAA	14	6	1	10	0	natriuretic peptide receptor A - guanylate cyclase A
92 AGCGATGAGA	9	10	0	0	0	ESTs
93 CGTGGGGTGT	9	10	17	3	0	ESTs

TEN's complete web table

Table 2. SAGE tags elevated in tumor endothelium. The top 46 tags with the highest tumor EC (T-EC's) to normal EC (N-EC's) tag ratios are listed in descending order. To calculate tag ratios, a value of 0.5 was assigned in cases where zero tags were observed. The SAGE libraries are the same as those listed in Table 1. Tag numbers for each group were normalized to 100,000 transcripts. A 'Description' of the gene product corresponding to each tag is given, followed by alternative names in parenthesis. If multiple tags for this gene are due to alternative polyadenylation sites, they are grouped together.

No.	Tag Sequence	N-EC's	T-EC's	HUVEC	HMVEC	Cell Lines	Description
1	GCGGCTGGCCA	0	28	0	2	0	ESTs, similarity to thrombomodulin 12M1
2	GATCTCCGCTGT	0	25	0	0	0	ESTs, similarity to rat Rhes ras-related protein 12M2
3	CATTTTATCT	0	23	0	0	0	ESTs
4	CTTCTCTTGAG	0	22	6	20	1	regulated in glioma-like 7-1 (DKK-3) REIC
5	TATTAACCTC	0	21	1	3	1	similar to JNK interacting protein-3a
6	CAGGABACCCC	0	16	2	0	0	MMP-11 (stromelysin 3)
7	GAAATGTCAA	1	31	53	22	1	MMP-2 (gelatinase A, 72kD type IV collagenase)
8	CTGGTTTCACT	0	15	0	0	0	ESTs
9	TTTTAAGAAC	0	14	1	4	0	ESTs
10	TTTGTTTTCC	5	139	0	16	0	collagen, type I, alpha 2, transcript A ^t
11	ATTTGTATGA	0	13	4	8	0	nitrogen (enattoin)
12	ACTTAGATGG	1	23	0	15	0	collagen, type VI, alpha 3
13	GAGTAGACGCC	3	63	0	0	1	Thy-1 cell surface antigen
14	GTACACACACC	0	10	0	0	0	ESTs / cytolin S
15	CCACAGGGAT	2	38	0	2	1	collagen, type III, alpha 1
16	TTAAAAGTAC	1	19	1	3	1	ESTs
17	ACAGACTGTTA	4	74	0	0	0	ESTs, similarity with sea squirt nitrogen 12M3
18	CCACTGCACCC	1	18	0	1	0	ESTs, similarity with homeobox protein DLX-3 12M4
19	CTATAGGAGC	1	18	1	1	0	ESTs, similarity with collagen, type I, alpha 2, transcript B ^t
20	GTTCACAGAA	0	9	0	3	0	ESTs / pregnancy specific beta-1-glycoprotein 1
21	TACCACTCTCC	0	9	4	1	1	end160 facin
22	GCCTTTCTCT	1	17	3	1	2	collagen, type I, alpha 1
23	TTAAATAGCAC	2	33	0	4	0	ESTs, DKK2P-A34G162 protein
24	AGACATACTGA	1	16	1	0	0	bone morphogenic protein 1 (metalloproteinase)
25	TCCCGAGGAG	1	16	0	0	0	slit (Drosophila) homolog 3 (MEGF5)
26	AGCCCCAAAGTG	0	8	0	0	0	KIAA0672 gene product
27	ACTACCATAAC	0	8	0	0	0	
28	TACAAATCGTT	0	8	0	0	0	

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28	TTGGGTAAAAA	0	8	0	0	ESTs
29	CATTATCAAA	0	8	0	0	integrin, alpha 1
30	AGAAACCAACGG	0	8	2	7	collagen, type IV, alpha 1
31	ACCAAAACAC	0	8	0	3	
32	TGAATAAAC	0	8	3	1	
G7	33	TTTGTTTCC	1	15	0	ESTs
34	GTGGAGAGGGA	1	15	1	2	ESTs
35	TTTGTTTGTAA	1	14	2	0	collagen, type XII, alpha 1
36	TTATGTTTAAAT	3	39	0	0	lumican
37	TGGAATGACC	15	179	0	40	ESTs / collagen, type I, alpha 1
38	TGCCACACAGT	1	18	0	2	transforming growth factor, beta 3
39	GATGAGGAGAC	3	35	0	18	collagen, type I, alpha 2, transcript C'
40	ATCAAAGGTTT	2	23	0	0	ESTs, DKFZp564O222 mRNA
41	AGTCACATAGT	1	11	2	0	cell division cycle 42 (GTP-binding protein)
42	TTCGGTTGGTC	4	45	0	19	
43	CCCGACACGGG	2	21	0	0	
44	GGCTTGCTTT	1	10	0	10	ESTs
45	ATCCCTTCGG	1	10	1	0	peanut-like protein 1
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Table 3. Detection of transcripts in various tumor types by RT-PCR and *In situ* hybridization (ISH). The "+" sign indicates the presence of a robust RT-PCR product or strong positive staining of vessels by *In situ* hybridization. The "-" sign indicates an undetectable signal by *In situ* hybridization or an absent or barely detectable transcript by RT-PCR. The "+/-" sign indicates a very weak signal in a limited number of vessels by *In situ* hybridization.

		TEM1	TEM3	TEM4	TEM5	TEM7	TEM8	TEM9	vWF	Hevin
RT-PCR	Colon Nor.	-	-	-	-	-	-	-	+	ND
	Colon Tum.	+	+	+	+	+	+	+	+	ND
ISH	Colon Nor.	-	-	-	-	-	-	-	+	+
	Colon Tum.	+	+	+	+	+	+	+	+	+
	Liver Met.	+	+/-	+	+	+	+	+	+/-	ND
	Lung Tum.	+	ND	+	+	+	+	+	+	+
	Brain Tum.	+	ND	ND	ND	+	ND	ND	+	*
	Corpus Lut.	+	+	+	+	-	-	+	+	+
	Wound	+	ND	+	ND	+/-	+/-	ND	+	+

* hevin was localized to both endothelial cells and malignant cells in brain tissue.

ND: not determined.

Table 3. SAGE tags elevated in normal endothelium. The top 46 tags with the highest normal EC (N-EC's) to tumor EC (T-EC's) tag ratios are listed in descending order. To calculate tag ratios, a value of 0.5 was assigned in cases where zero tags were observed. The SAGE libraries are the same as those listed in Table 1. Tag numbers for each group were normalized to 100,000 transcripts. A 'Description' of the gene product corresponding to each tag is given, followed by alternative names in parenthesis.

no.	Tag Sequence	N-EC's	T-EC's	HUVEC	HMVEC Cell Lines	Description
1	TCTCAGCTCT	28	0	0	0	mucosal vascular addressin cell adhesion molecule 1
2	CTAGCGTTT	19	0	4	14	serum deprivation response (phosphatidylserine-binding protein)
3	GTCGCTGACG	18	0	1	0	ESTs / intercellular adhesion molecule 4
4	CTCTAAAAAA	34	1	1	0	small inducible cytokine subfamily A (Cys-Cys), member 14
5	TGGGAAGAGG	16	0	3	4	ESTs
6	GTTAAAGAT	16	0	0	0	ESTs / endothelin 1 / ribosomal protein L27
7	CTTGTGTTG	15	0	56	32	TU3A protein
8	ATTGCCATC	14	0	0	4	selectin E (endothelial adhesion molecule 1)
9	TGTTGAAAAA	21	1	0	0	TU3A protein
10	ACAAAAAGGC	21	1	0	6	phosphodiesterase 1 - nucleotide pyrophosphatase 2 (autotaxin)
11	AAGATGACAC	21	1	1	1	platelet/endothelial cell adhesion molecule (CD31 antigen)
12	GTAGGGAAA	10	0	0	9	ESTs
13	TGTTCAAGG	10	0	0	0	ESTs / small inducible cytokine subfamily A, member 14
14	CTCTTCAAAA	19	1	1	0	transforming growth factor, beta receptor II (70-80kD)
15	TATTTAAATA	18	1	6	9	ESTs
16	GAATTCCACA	9	0	1	14	small inducible cytokine subfamily A, member 14
17	AAGGAAACT	9	0	0	0	active BCR-related gene
18	AATATCTGAC	9	0	2	2	protein kinase C eta
19	TCAGTGACAG	17	1	4	7	ESTs
20	GCAAAGTGCC	32	2	1	5	ESTs (2 unigene clusters)
21	TAATATCTTG	8	0	2	0	ESTs
22	GTCACTATT	8	0	1	0	ESTs
23	ATAACCTGCA	8	0	0	0	signaling lymphocytic activation molecule
24	TGGATCTGTGC	46	3	1	1	ESTs / glycogenin 2
25	TAAGGGACAA	15	1	4	3	LIM binding domain 2
26	GACGGCGGGCT	73	5	11	7	claudin 5
27	ACTCCGGTGT	14	1	0	8	ESTs

28	CTTCTCACCT	27	2	3	1
29	TGTTGCTTGG	13	1	0	0
30	GAGGAGTCT	13	1	4	2
31	CTCTAAAAAA	10	1	0	1
32	GAAACCGGT	10	1	0	0
33	AACACAGTGCG	10	1	7	15

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From page N^o 77 - 305 are sequence
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